



**Supplementary Figure 7. Read length distribution profiles vary between sRNA-seq datasets.** We downloaded publicly available sRNA-seq datasets from the NCBI SRA database at <https://www.ncbi.nlm.nih.gov/sra> (accessions summarized in Supplementary Table 8) and analyzed the read length profiles of reads between 15 and 40 bases in length. The x-axis shows number of reads and the y-axis the read length in bases. We examined datasets from the following samples: **(A)** *H. vulgare* infected with *B. hordei* at 0, 24, and 48 hpi (Hunt *et al.* 2019); **(B)** *H. vulgare* under salt stress (Deng *et al.* 2015) and aluminium stress (Wu *et al.* 2018), respectively; **(C)** *Triticum aestivum* (wheat) after infection with *B. graminis* f.sp. *tritici* at 12 hpi and under 40 °C heat stress (Xin *et al.* 2011); **(D)** *T. aestivum* infected with *Zymoseptoria tritici* at 12 dpi (Ma *et al.* 2019); **(E)** *T. aestivum* under 37 °C heat stress, continuous light stress, or UV treatment stress (Ragupathy *et al.* 2016); **(F)** *Glycine max* (soybean) during nodulation with the bacterial species *Bradyrhizobium japonicum* at 10 and 20 days after inoculation (Ren *et al.* 2019); **(G)** *Arabidopsis thaliana* and *Phaseolus vulgaris* (common bean) during infection with *Sclerotinia sclerotiorum* (Derbyshire *et al.* 2019); **(H)** *A. thaliana* after infection with *Verticillium dahliae* and the *V. dahliae* mutant *aly1 aly2* (Zhu *et al.* 2022); **(I)** *A. thaliana* infected with *Hyaloperonospora arabidopsidis* at 3, 4, and 7 dpi (Dunker *et al.* 2020); **(J)** *Botrytis cinerea* cultivated *in vitro* (Weiberg *et al.* 2013); **(K)** *A. thaliana* infected with *B. cinerea* at 24, 48, and 72 hpi (Weiberg *et al.* 2013).